FIGURE 1
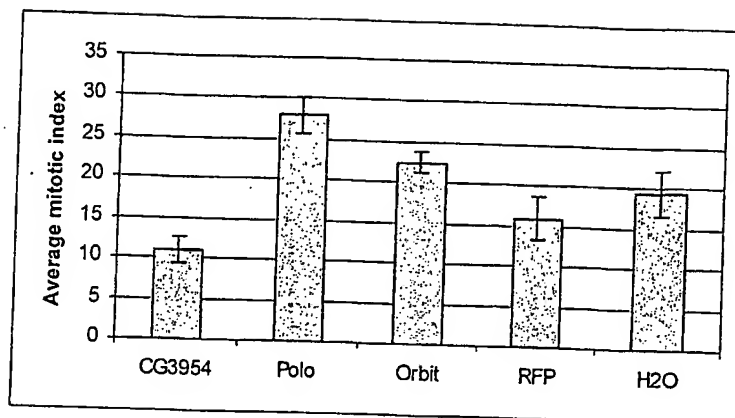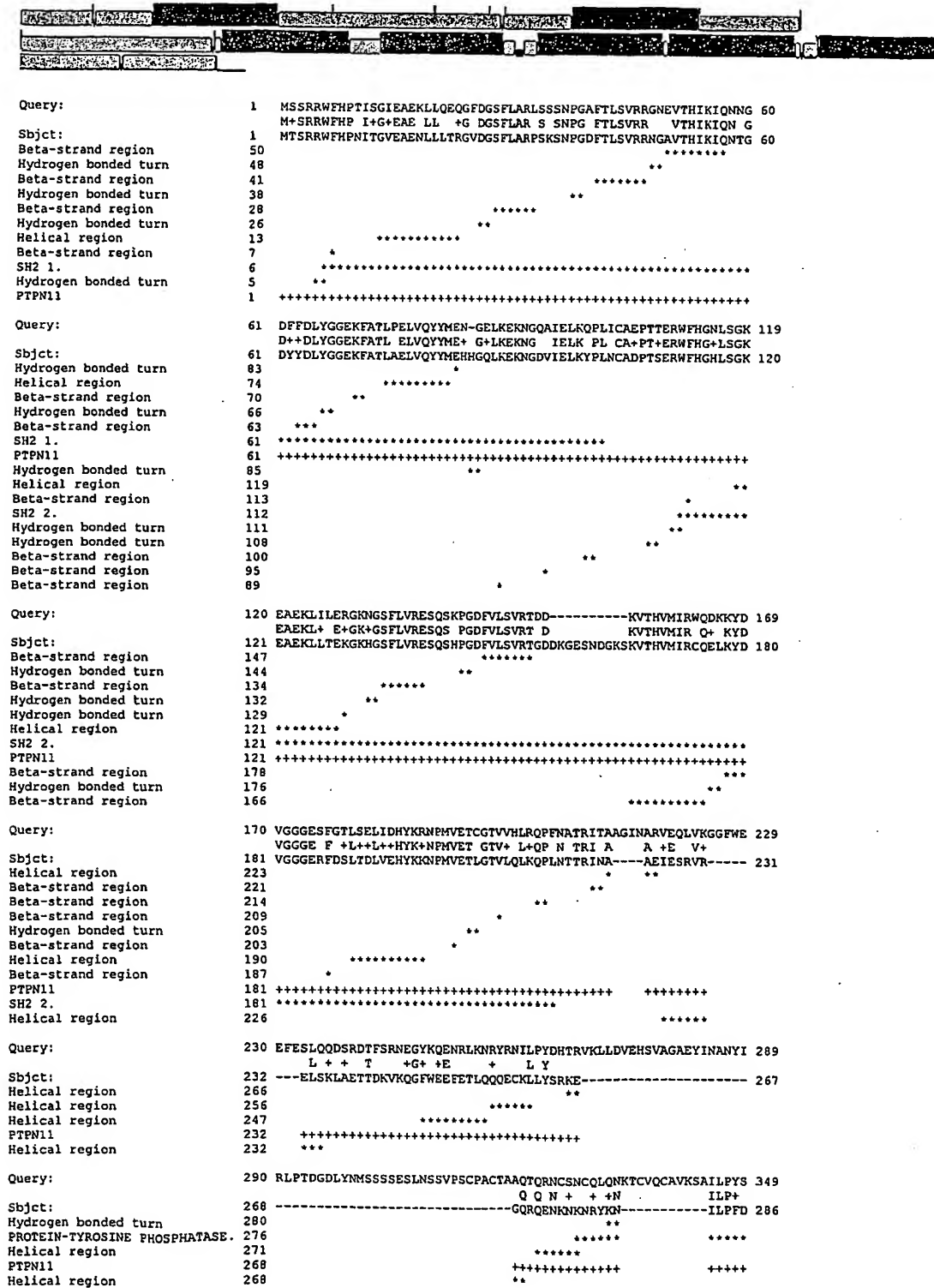
FIGURE 2

```
Score = 553 bits (1425), Expect = e-156
Identities = 327/700 (46%), Positives = 406/700 (57%), Gaps = 152/700 (21%)
```



```
Query:                        1   MSSRRWFHPTISGIEAEKLLQEQGFDGSFLARLSSSNPGAFTLSVRRGNEVTHIKIQNNG 60
                                  M+SRRWFHP I+G+EAE LL  +G DGSFLAR S SNPG FTLSVRR    VTHIKIQN G
Sbjct:                        1   MTSRRWFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDFTLSVRRNGAVTHIKIQNTG 60
Beta-strand region           50                                                    ********
Hydrogen bonded turn         48                                                          **
Beta-strand region           41                                             *******
Hydrogen bonded turn         38                                           **
Beta-strand region           28                                    ******
Hydrogen bonded turn         26                                  **
Helical region               13                      **********
Beta-strand region           7                  *
SH2 1.                       6                  ********************************************
Hydrogen bonded turn         5      **
PTPN11                       1   +++++++++++++++++++++++++++++++++++++++++++++++++++++++++++

Query:                       61  DFFDLYGGEKFATLPELVQYYMEN-GELKEKNGQAIELKQPLICAEPTTERWFHGNLSGK 119
                                 D++DLYGGEKFATL ELVQYYME+ G+LKEKNG  IELK PL CA+PT+ERWFHG+LSGK
Sbjct:                       61  DYYDLYGGEKFATLAELVQYYMEHHGQLKEKNGDVIELKYPLNCADPTSERWFHGHLSGK 120
Hydrogen bonded turn         83                             *
Helical region               74                        *********
Beta-strand region           70                     **
Hydrogen bonded turn         66                   **
Beta-strand region           63                  ***
SH2 1.                       61  *******************************************
PTPN11                       61  +++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
Hydrogen bonded turn         85                                     **
Helical region              119                                                           **
Beta-strand region          113                                                          *
SH2 2.                      112                                                     *********
Hydrogen bonded turn        111                                                       **
Hydrogen bonded turn        108                                                  **
Beta-strand region          100                                            **
Beta-strand region           95                                      *
Beta-strand region           89                                 *

Query:                      120 EAEKLILERGKNGSFLVRESQSKPGDFVLSVRTDD----------KVTHVMIRWQDKKYD 169
                                EAEKL E+GK+GSFLVRESQS PGDFVLSVRT D          KVTHVMIR Q+ KYD
Sbjct:                      121 EAEKLLTEKGKHGSFLVRESQSHPGDFVLSVRTGDDKGESNDGKSKVTHVMIRCQELKYD 180
Beta-strand region          147                            *******
Hydrogen bonded turn        144                          **
Beta-strand region          134                     ******
Hydrogen bonded turn        132                   **
Hydrogen bonded turn        129                 *
Helical region              121 ********
SH2 2.                      121 ****************************************************
PTPN11                      121 +++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
Beta-strand region          178                                                         ***
Hydrogen bonded turn        176             .                                          **
Beta-strand region          166                                             **********

Query:                      170 VGGGESFGTLSELIDHYKRNPMVETCGTVVHLRQPFNATRITAAGINARVEQLVKGGFWE 229
                                VGGGE F +L++L++HYK+NPMVET GTV+ L+QP N TRI A   A +E V+
Sbjct:                      181 VGGGERFDSLTDLVEHYKKNPMVETLGTVLQLKQPLNTTRINA----AEIESRVR----- 231
Helical region              223                                            *    **
Beta-strand region          221                                           *
Beta-strand region          214                                       **   **
Beta-strand region          209                                     *
Hydrogen bonded turn        205                                 **
Beta-strand region          203                               *
Helical region              190                 **********
Beta-strand region          187              *
PTPN11                      181 +++++++++++++++++++++++++++++++++++++++++     ++++++++
SH2 2.                      181 *************************************
Helical region              226                                             ******

Query:                      230 EFESLQQDSRDTFSRNEGYKQENRLKNRYRNILPYDHTRVKLLDVEHSVAGAEYINANYI 289
                                 L + + T    +G+ +E    +  L Y
Sbjct:                      232 ---ELSKLAETTDKVKQGFWEEFETLQQQECKLLYSRKE-------------------- 267
Helical region              266                                    **
Helical region              256                             ******
Helical region              247                     *********
PTPN11                      232     +++++++++++++++++++++++++++++++++++
Helical region              232 ***

Query:                      290 RLPTDGDLYNMSSSSESLNSSVPSCPACTAAQTQRNCSNCQLQNKTCVQCAVKSAILPYS 349
                                              Q Q N +  + +N         ILP+
Sbjct:                      268 ----------------------------GQRQENKNKNRYKN-----------ILPFD 286
Hydrogen bonded turn        280                                       **
PROTEIN-TYROSINE PHOSPHATASE. 276                                  ******        *****
Helical region              271                                 ******
PTPN11                      268                              +++++++++++++      ++++
Helical region              268                              **
```

```
Hydrogen bonded turn              286

Query:                           350 NCATCSRKSDSLSKHHKRSESSASSSPSSGSGSGPGSSGTSGVSSVNGPGTPTNLTSGTAG 409
                                     +      D                                      P    P +
Sbjct:                           287 HTRVVLHDGD------------------------------------PNEPVS------- 302
Beta-strand region               289   ***
Hydrogen bonded turn             287 **
PTPN11                           287 ++++++++++                                      ++++++
PROTEIN-TYROSINE PHOSPHATASE.    287 **********                                      ******

Query:                           410 CLVGLLKRHSNDSSGAVSISMAERERE-REREMFKTYIATQGCLLTQQVNTVTDFWNMVW 468
                                         D   A +I M E E +     +  K+YIATQGCL    NTV DFW MV+
Sbjct:                           303 -----------DYINA-NIIMPEFETKCHNSKPKKSYIATQGCLQ----NTVNDFWRMVF 346
Beta-strand region               304            ****  ***
PTPN11                           303            +++++ +++++++++++++++++++++++++++    ++++++++++++
PROTEIN-TYROSINE PHOSPHATASE.    303            ***** ****************************    *  **
Hydrogen bonded turn             335                                                 *     **
Beta-strand region               327                                            ****  .
Helical region                   338                                                      *********

Query:                           469 QENTRVIVMTTKEYERGKEKCARYWPDEGRSEQFGHARIQCVSENSTSDYTLREFLVSWR 528
                                     QEN+RVIVMTTKE ERGK KC +YWPDE   +++G  R++ V E++   DYTLRE  +S
Sbjct:                           347 QENSRVIVMTTKEVERGKSKCVKYWPDEYALKEYGVMRVRNVKESAAHDYTLRELKLSKV 406
Hydrogen bonded turn             406                                                      *
Beta-strand region               396                                            **********
Beta-strand region               383                                         **
Hydrogen bonded turn             381                                   ****
Beta-strand region               377                               **
Hydrogen bonded turn             374                    **
Beta-strand region               364                  **
Hydrogen bonded turn             362                **
Beta-strand region               360              **
Beta-strand region               352        ****
Hydrogen bonded turn             349   *
Helical region                   347 **
PTPN11                           347 +++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
PROTEIN-TYROSINE PHOSPHATASE.    347 ***********************************************************

Query:                           529 DQ--PARRIFHYHFQVWPDHGVPADPGCVLNFLQDVNTRQSHLAQAGEKPGPICVHCSAG 586
                                      Q     R ++ YHF+ WPDHGVP+DPG VL+FL++V+ +Q  +  AG    P+ VHCSAG
Sbjct:                           407 GQGNTERTVWQYHFRTWPDHGVPSDPGGVLDFLEEVHHKQESIMDAG----PVVVHCSAG 462
Beta-strand region               408 *************
Hydrogen bonded turn             407 *
PTPN11                           407 +++++++++++++++++++++++++++++++++++ +++++++++++++    ++++++++++
PROTEIN-TYROSINE PHOSPHATASE.    407 *************************************************    *********
Hydrogen bonded turn             450                                             **
Helical region                   432                              *****************
active                           459
Beta-strand region               455                                                      ****

Query:                           587 IGRTGTFIVIDMILDQIVRNGLDTEIDIQRTIQMVRSQRSGLVQTEAQYKFVYYAVQHYI 646
                                     IGRTGTFIVID+++D I    G+D +ID+ +TIQMVRSQRSG+VQTEAQY+F+Y AVQHYI
Sbjct:                           463 IGRTGTFIVIDILIDIIREKGVDCDIDVPKTIQMVRSQRSGMVQTEAQYRFIYMAVQHYI 522
Helical region                   508                                                 **************
Hydrogen bonded turn             502                                                  **
Hydrogen bonded turn             499                                              **
Helical region                   490                                    *********
Beta-strand region               487                                  **
Hydrogen bonded turn             484                               **
Helical region                   464 ******************
PTPN11                           463 +++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
PROTEIN-TYROSINE PHOSPHATASE.    463 ***********************************************************

Query:                           647 QTLIARKRAEEQSLQVGREYTNIKYTGEIGNDSQRSPLPP 686
                                     +TL  R   E++S + G EYTNIKY+        +SPLPP
Sbjct:                           523 ETLQRRIEEEQKSKRKGHEYTNIKYSLADQTSGDQSPLPP 562
Conflict                         548                             *
phosphorylation                  542                          *
Conflict                         535                 *
Hydrogen bonded turn             524 *
Helical region                   523 *
PTPN11                           523 +++++++++++++++++++++++++++++++++++++++
```
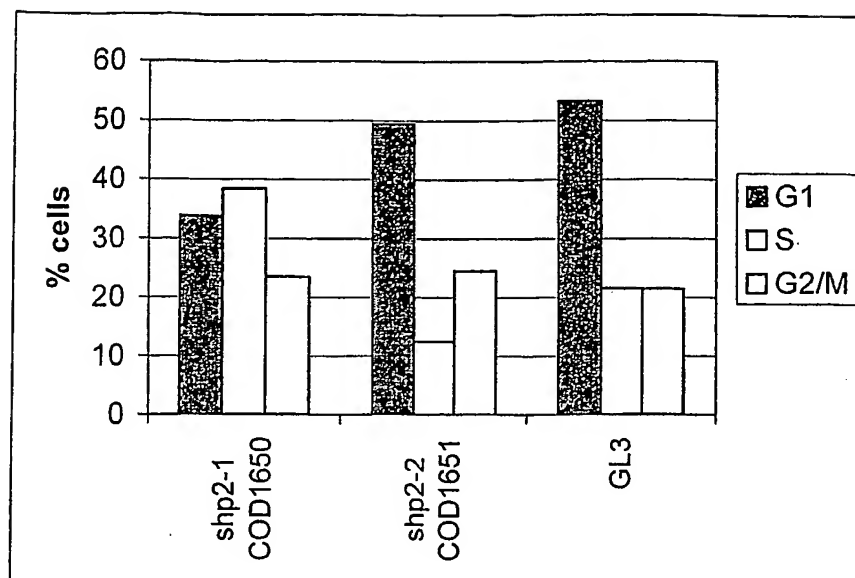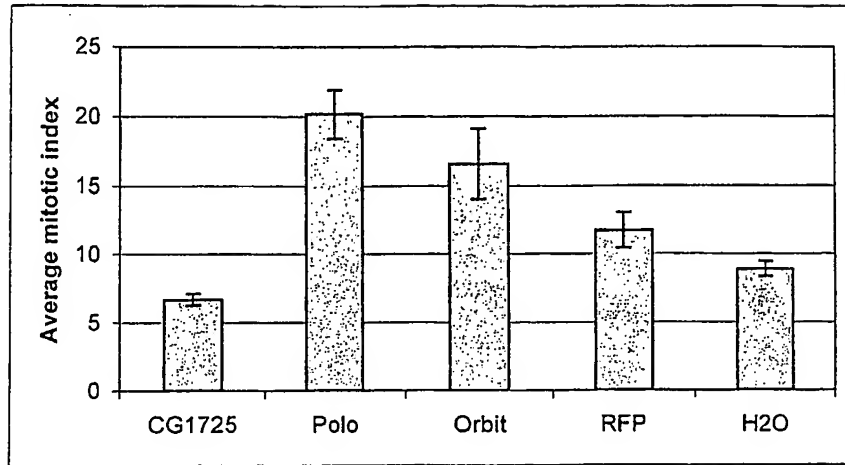
FIGURE 3

FIGURE 4

FIGURE 5

FIGURE 6A

Sequence alignment of Dros Dlg1 and Hu Dlg homolog 1

BLAST P sequence alignment

Score = 616 bits (1588), Expect = e-175
Identities = 306/517 (59%), Positives = 390/517 (75%), Gaps = 24/517 (4%)


```
Query: 453 QPGSRYASTNVLAAVPPGTPRAVST--------EDITREPRTITIQKGPQGLGFNIVGGE 504
           QP  + S +      P +P  S        ++ITREPR + + +G  GLGFNIVGGE
Sbjct: 425 QPVDNHVSPSSFLGQTPASPARYSPVSKAVLGDDEITREPRKVVLHRGSTGLGFNIVGGE 484

Query: 505 DGQGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTLLAQ 564
           DG+GI++SFILAGGPADL  EL++GD+++SVN+V+L  A+HE+AA ALK +G  VT++AQ
Sbjct: 485 DGEGIFISFILAGGPADLSGELRKGDRIISVNSVDLRAASHEQAAAALKNAGQAVTIVAQ 544

Query: 565 YRPEEYNRFEARIQELKQQXXXXXXXXXXXXX-XXQKRSLYVRALFDYDPNRDDGLPSRG 623
           YRPEEY+RFEA+I +L++Q                QKRSLYVRALFDYD +D GLPS+G
Sbjct: 545 YRPEEYSRFEAKIHDLREQMMNSSISSGSGSLRTSQKRSLYVRALFDYDKTKDSGLPSQG 604

Query: 624 LPFKHGDILHVTNASDDEWWQARRVLGDNEDEQIGIVPSKRRWERKMRARDRSVKFQGHA 683
           L FK GDILHV NASDDEWWQAR+V  D E +++G++PSKRR E+K RAR ++VKF
Sbjct: 605 LNFKFGDILHVINASDDEWWQARQVTPDGESDEVGVIPSKRRVEKKERARLKTVKFN--- 661

Query: 684 AANNNLDKQSTLDRKKKNFTFSRKFPFMKSRDEKNEDGSDQEPNGVVSSTSEIDIXXXXX 743
           +   DK + + K+K  FSRKFPF K++D+  ++ SD + + V S+ S+ +
Sbjct: 662 --SKTRDKGQSFNDKRKKNLFSRKFPFYKNKDQSEQETSDADQH-VTSNASDSE------ 712

Query: 744 XXXXXXXXXXXXXVLSYEAVQRLSINYTRPVIILGPLKDRINDDLISEYPDKFGSCVPHTT 803
                        VLSYE V +  +NYTRPVIILGP+KDRINDDLISE+PDKFGSCVPHTT
Sbjct: 713 ---SSYRGQEEYVLSYEPVNQQEVNYTRPVIILGPMKDRINDDLISEFPDKFGSCVPHTT 769

Query: 804 RPKREYEVDGRDYHFVSSREQMERDIQNHLFIEAGQYNDNLYGTSVASVREVAEKGKHCI 863
           RPKR+YEVDGRDYHFV+SREQME+DIQ H FIEAGQYN++LYGTSV SVREVA KGKHCI
Sbjct: 770 RPKRDYEVDGRDYHFVTSREQMEKDIQEHKFIEAGQYNNHLYGTSVQSVREVAGKGKHCI 829

Query: 864 LDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRMTEEQAKKTYERAIKMEQEFGEY 923
           LDVSGNAIKRLQ+AQLYP+++FIKPKS++++MEMN+R+TEEQA+KT+ERA+K+EQEF E+
Sbjct: 830 LDVSGNAIKRLQIAQLYPISIFIKPKSMENIMEMNKRLTEEQARKTFERAMKLEQEFTEH 889

Query: 924 FTGVVQGDTIEEIYSKVKSMIWSQSGPTIWVPSKESL 960
           FT +VQGDT+E+IY++VK +I  QSG  IWVP+KE L
Sbjct: 890 FTAIVQGDTLEDIYNQVKQIIEEQSGSYIWVPAKEKL 926
```
Score = 206 bits (524), Expect = 2e-51
Identities = 119/227 (52%), Positives = 146/227 (63%), Gaps = 30/227 (13%)


```
Query:  24 LFNLDS------VNGDDS-WLYEDIQLERGNSGLGFSIAGGTDNPHIGTDTSIYITKLIS 76
           L N DS       VNG D+ + YE+I LERGNSGLGFSIAGGTDNPHIG D+SI+ITK+I+
Sbjct: 201 LVNTDSLETPTYVNGTDADYEYEEITLERGNSGLGFSIAGGTDNPHIGDDSSIFITKIIT 260

Query:  77 GGAAAADGRLXXXXXXXXXXXXXXXXXXXXPHASAVDALKKAGNVVKLHVKRKXXXXXXXXXX 136
           GGAAA DGRL            H+ AV+ALK+AG++V+L+VKR+
Sbjct: 261 GGAAAQDGRLRVNDCILQVNEVDVRDVTHSKAVEALKEAGSIVRLYVKRRKPVSE----- 315

Query: 137 XXXXXXXXXXXXXXXKVIEIDLVKGGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRAQV 196
                          K++EI L+KG KGLGFSIAGG+GNQHIPGDN IYVTK+ +GG A
Sbjct: 316 --------------KIMEIKLIKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHK 361
```

```
Query: 197 DGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLIIGK 243
           DG+L IGDKL+AV    +   LE VTHE AV  LK+ +D V L + K
Sbjct: 362 DGKLQIGDKLLAV----NNVCLEEVTHEEAVTALKNTSDFVYLKVAK 404
Score = 88.2 bits (217), Expect = 7e-16
Identities = 68/234 (29%), Positives = 95/234 (40%), Gaps = 43/234 (18%)
```



```
Query: 40  DIQLERGNSGLGFSIAGGTDNPHIGTDTSIYITKLISGGAAAADGRLXXXXXXXXXXXXX 99
           +I+L +G  GLGFSIAGG N HI  D SIY+TK+I GGAA  DG+L
Sbjct: 319 EIKLIKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGKLQIGDKLLAVNNVC 378

Query: 100 XXXXPHASAVDALKKAGNVVKLHVKRKXXXXXXXXXXXXXXXXXXXXXXXXXXXKVI------ 153
               H  AV ALK   + V L V +                             V
Sbjct: 379 LEEVTHEEAVTALKNTSDFVYLKVAKPTSMYMNDGYAPPDITNSSSQPVDNHVSPSSFLG 438

Query: 154 ------------------------EIDLVKGGKGLGFSIAGGIGNQHIPGDNGIYVT 186
                                   ++ L +G GLGF+I GG  +     GI+++
Sbjct: 439 QTPASPARYSPVSKAVLGDDEITREPRKVVLHRGSTGLGFNIVGGEDGE------GIFIS 492

Query: 187 KLTDGGRAQVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLI 240
           +  GG A + G L  GD++I+V    + +L   +HE A A LK+   VT++
Sbjct: 493 FILAGGPADLSGELRKGDRIISV----NSVDLRAASHEQAAAALKNAGQAVTIV 542
Score = 70.1 bits (170), Expect = 2e-10
Identities = 47/141 (33%), Positives = 69/141 (48%), Gaps = 12/141 (8%)
```



```
Query: 432 MPALPVESNQTNNRSQSPQPRQPGSRYASTNVLAAVPPGTPRAVSTEDITREPRTITIQK 491
           +P LPV +  T      PQ  P    +T+ L   TP V+ D  E  IT+++
Sbjct: 176 IPVLPVPAENTVILPTIPQANPPPV-LVNTDSLE-----TPTYVNGTDADYEYEEITLER 229

Query: 492 GPQGLGFNIVGGEDG------QGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATH 545
           G  GLGF+I GG D        I+++ I+ GG A    L+  D +L VN V++    TH
Sbjct: 230 GNSGLGFSIAGGTDNPHIGDDSSIFITKIITGGAAAQDGRLRVNDCILQVNEVDVRDVTH 289

Query: 546 EEAAQALKTSGGVVTLLAQYR 566
           +A +ALK +G +V L  + R
Sbjct: 290 SKAVEALKEAGSIVRLYVKRR 310
Score = 67.4 bits (163), Expect = 1e-09
Identities = 39/81 (48%), Positives = 49/81 (60%), Gaps = 6/81 (7%)
```



```
Query: 487 ITIQKGPQGLGFNIVGGEDGQ------GIYVSFILAGGPADLGSELKRGDQLLSVNNVNL 540
           I + KGP+GLGF+I GG  Q       IYV+ I+ GG A   +L+ GD+LL+VNNV L
Sbjct: 320 IKLIKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGKLQIGDKLLAVNNVCL 379

Query: 541 THATHEEAAQALKTSGGVVTL 561
           THEEA  ALK +   V L
Sbjct: 380 EEVTHEEAVTALKNTSDFVYL 400
```

FIGURE 6B

CLUSTAL W (1.82) sequence alignment

```
Drosophila   MTTRKKKRDGGGSGGGFIKKVSSLFNLDSVNGDDSWLYEDIQLERGNSGLGFSIAGGTDN 60
Human        MPVRKQD-----------TQRALHLLEEYRSKLSQTEDRQLRSSIERVINIFQSNLFQ 47
             *..**:.              .. ::*  .  ..  ** **. . . :   :  .. :

Drosophila   PHIGTDTSIYITKLISGGAAAADGRLSINDIIVSVNDVSVVDVPHASAVDALKKAGNVVK 120
Human        ALIDIQEFYEVTLLDN--PKCID-RSKPSEPIQPVNTWEISSLPSSTVTSETLPSSLSPS 104
             . *. :    :* * .  .. * * . .: * .** .: .:* ::...    :.  .

Drosophila   LHVKRKRGTATTPAAGSAAGDARDSAASGPKVIEIDLVKGGKGLGFSIAGGIGNQHIPGD 180
Human        VEKYRYQDEDTPPQEHISP--QITNEVIGPELVHVSEKN--LSEIENVHGFVSHSHIS-P 159
             :. * :. *.*  :.   . . **::.:. :   .  .: * :.:.**.

Drosophila   NGIYVTKLTDGGRAQVDGRLSIGDKLIAVRTNGSEKN---LENVTHELAVATLKSITDKV 237
Human        IKPTEAVLPSPPTVPVIPVLPVPAENTVILPTIPQANPPPVLVNTDSLETPTYVNGTDAD 219
             : *..  . * *.: : .: .. .: *  :  *..* ..* . **

Drosophila   TLIIGKTQHLTTSAS----GGGGGGLSSGQQLSQSQSQLATSQSQSQVHQQQHATPMVNS 293
Human        YEYEEITLERGNSGLGFSIAGGTDNPHIGDDSSIFITKIITGGAAAQDGRLRVNDCILQV 279
             *  . .*.     .** ..  *:: *  :::  *. : :*  : :    :::

Drosophila   QSTGALNSMGQTVVDSPSIPQAAAAVAAAANASASASVIASNNTISNTTVTTVTATATAS 353
Human        NEVDVRDVTHSKAVEALKEAGSIVRLYVKRRKPVSEKIMEIK-LIKGPKGLGFSIAGGVG 338
             :.... :   ...*:: . . : .. .  ...* .:: :  *.... .: :. ..

Drosophila   NDSSKLPPSLGANSSISISNSNSNSNSNNINNINSINNNNSSSSSTTATVAAATPTAASA 413
Human        NQHIPGDNSIYVTKIIEGGAAHKDGKLQIGDKLLAVNNVCLEEVTHEEAVTALKNTSDFV 398
             *:     *: ... *. . ::.:.: : ::: ::**  .. :   :*:* . *:  .

Drosophila   AAAAASSPPANSFYNNASMPALPVESNQTNNRSQSPQPRQPGSRYASTNVLAAVPPGTPR 473
Human        YLKVAK-PTSMYMNDGYAPPDITNSSSQPVDNHVSPSS-FLGQTPASP---ARYSPVSKA 453
             .*. *.: .: :. : * :. ..*.*. :. **.. *. **. * .* :

Drosophila   AVSTEDITREPRTITIQKGPQGLGFNIVGGEDGQGIYVSFILAGGPADLGSELKRGDQLL 533
Human        VLGDDEITREPRKVVLHRGSTGLGFNIVGGEDGEGIFISFILAGGPADLSGELRKGDRII 513
             .:. ::******.:.::*. ************:**:************..**::**::: 

Drosophila   SVNNVNLTHATHEEAAQALKTSGGVVTLLAQYRPEEYNRFEARIQELKQQAALGAGGSGT 593
Human        SVNSVDLRAASHEQAAAALKNAGQAVTIVAQYRPEEYSRFEAKIHDLREQMMNSSISSGS 573
             ***.*:* *:**:** ***.:* .**::********.****:*::*::*  .: .**: 

Drosophila   -LLRTTQKRSLYVRALFDYDPNRDDGLPSRGLPFKHGDILHVTNASDDEWWQARRVLGDN 652
Human        GSLRTSQKRSLYVRALFDYDKTKDSGLPSQGLNFKFGDILHVINASDDEWWQARQVTPDG 633
             ***:************** .:* .****:** ** ****** ***********:* *.

Drosophila   EDEQIGIVPSKRRWERKMRARDRSVKFQGHAAANNNLDKQSTLDRKKKNFTFSRKFPFMK 712
Human        ESDEVGVIPSKRRVEKKERARLKTVKFN-----SKTRDKGQSFNDKRKKNLFSRKFPFYK 688
             *.:::*::***** *:* *** ::***:       :. ** .::: *:*: ******* *

Drosophila   SRDEKNEDGSDQEPNGVVSSTSEIDINNVNNNQSNEPQPSEENVLSYEAVQRLSINYTRP 772
Human        NKDQSEQETSDADQH-VTSNASDSESSYRGQ---------EEYVLSYEPVNQQEVNYTRP 738
             .:*:.::: ** : : *.*.:*: : . .:          ** *****.*:: .:*****

Drosophila   VIILGPLKDRINDDLISEYPDKFGSCVPHTTRPKREYEVDGRDYHFVSSREQMERDIQNH 832
Human        VIILGPMKDRINDDLISEFPDKFGSCVPHTTRPKRDYEVDGRDYHFVTSREQMEKDIQEH 798
             ******:***********:****************:***********:*****:***:*.

Drosophila   LFIEAGQYNDNLYGTSVASVREVAEKGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVD 892
Human        KFIEAGQYNNHLYGTSVQSVREVAGKGKHCILDVSGNAIKRLQIAQLYPISIFIKPKSME 858
             ********:::****** ****** *******************:*****::.******::

Drosophila   SVMEMNRRMTEEQAKKTYERAIKMEQEFGEYFTGVVQGDTIEEIYSKVKSMIWSQSGPTI 952
Human        NIMEMNKRLTEEQARKTFERAMKLEQEFTEHFTAIVQGDTLEDIYNQVKQIIEEQSGSYI 918
             .:****:*:*****:**:***:*:**** *:**.:*****:*:**:.**::*:**.* *
```

```
Drosophila    WVPSKESL 960
Human         WVPAKEKL 926
              ***:**.*
```

FIGURE 6C

Sequence alignment of Dros Dlg1 and Hu Dlg homolog 2

BLASTP sequence alignment

```
Score =  621 bits (1601), Expect = e-176
Identities = 318/524 (60%), Positives = 390/524 (73%), Gaps = 43/524 (8%)
```



```
Query: 438 ESNQTNNRSQSPQPRQPGSRYASTNVLAAVPPGTPRAVSTEDITREPRTITIQKGPQGLG 497
               +S. T++  S  RQP                 RAVS E   EPR + + KG  GLG
Sbjct: 389 DSEMTSHSQHSTATRQPSMTLQ-------------RAVSLEG---EPRKVVLHKGSTGLG 432

Query: 498 FNIVGGEDGQGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGG 557
               FNIVGGEDG+GI+VSFILAGGPADL  EL+RGDQ+LSVN ++L  A+HE+AA ALK +G
Sbjct: 433 FNIVGGEDGEGIFVSFILAGGPADLSGELQRGDQILSVNGIDLRGASHEQAAAALKGAGQ 492

Query: 558 VVTLLAQYRPEEYNRFEARIQELKQQXXXXXXXXXXXXXXX-QKRSLYVRALFDYDPNRD 616
               VT++AQY+PE+Y RFEA+I +L++Q                QKRSLYVRA+FDYD ++D
Sbjct: 493 TVTIIAQYQPEDYARFEAKIHDLREQMMNHSMSSGSGSLRTNQKRSLYVRAMFDYDKSKD 552

Query: 617 DGLPSRGLPFKHGDILHVTNASDDEWWQARRVLGDNEDEQIGIVPSKRRWERKMRARDRS 676
               GLPS+GL FK+GDILHV NASDDEWWQARRV+ + + E++G++PSKRR ERK RAR ++
Sbjct: 553 SGLPSQGLSFKYGDILHVINASDDEWWQARRVMLEGDSEEMGVIPSKRRVERKERARLKT 612

Query: 677 VKFQGHAAANNNLDKQSTLDRKKKNFTFSRKFPFMKSRDEKNEDGSDQEPNGVVSSTSEI 736
               VKF        ++  K S  D++KK+F FSRKFPF K++++  ++ SD E       · +
Sbjct: 613 VKFNAKPGVIDS--KGSFNDKRKKSFIFSRKFPFYKNKEQSEQETSDPE-------RGQE 663

Query: 737 DIXXXXXXXXXXXXXXXXXXXVLSYEAVQRLSINYTRPVIILGPLKDRINDDLISEYPDKFG 796
               D+                    +LSYE V R  INYTRPVIILGP+KDRINDDLISE+PDKFG
Sbjct: 664 DL-----------------ILSYEPVTRQEINYTRPVIILGPMKDRINDDLISEFPDKFG 706

Query: 797 SCVPHTTRPKREYEVDGRDYHFVSSREQMERDIQNHLFIEAGQYNDNLYGTSVASVREVA 856
               SCVPHTTRPKR+YEVDGRDYHFV SREQME+DIQ H FIEAGQYNDNLYGTSV SVR VA
Sbjct: 707 SCVPHTTRPKRDYEVDGRDYHFVISREQMEKDIQEHKFIEAGQYNDNLYGTSVQSVRFVA 766

Query: 857 EKGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRMTEEQAKKTYERAIKM 916
               E+GKHCILDVSGNAIKRLQVAQLYP+A+FIKP+S++S+MEMN+R+TEEQAKKTY+RAIK+
Sbjct: 767 ERGKHCILDVSGNAIKRLQVAQLYPIAIFIKPRSLESLMEMNKRLTEEQAKKTYDRAIKL 826

Query: 917 EQEFGEYFTGVVQGDTIEEIYSKVKSMIWSQSGPTIWVPSKESL 960
               EQEFGEYFT +VQGDT+E+IY++ K +I  QSGP IW+PSKE L
Sbjct: 827 EQEFGEYFTAIVQGDTLEDIYNQCKLVIEEQSGPFIWIPSKEKL 870
Score =  197 bits (502), Expect = 7e-49
Identities = 111/221 (50%), Positives =·140/221 (63%), Gaps = 24/221 (10%)
```



```
Query: 23  SLFNLDSVNGDD-SWLYEDIQLERGNSGLGFSIAGGTDNPHIGTDTSIYITKLISGGAAA 81
               +L +  VNG +  + +E+I LERGNSGLGFSIAGGTDNPHIG D  I+ITK+I GGAAA
Sbjct: 80  TLDTIPYVNGTEIEYEFEEITLERGNSGLGFSIAGGTDNPHIGDDPGIFITKIIPGGAAA 139

Query: 82  ADGRLXXXXXXXXXXXXXXXXXXXPHASAVDALKKAGNVVKLHVKRKXXXXXXXXXXXXXXXX 141
               DGRL                   H+ AV+ALK+AG++ +L+V+R+
Sbjct: 140 EDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARLYVRRRRPILET--------- 190

Query: 142 XXXXXXXXXXKVIEIDLVKGGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRAQVDGRLS 201
```

```
                      V+EI L KG KGLGFSIAGG+GNQHIPGDN IYVTK+ DGG AQ DGRL
Sbjct: 191 ----------VVEIKLFKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIDGGAAQKDGRLQ 240

Query: 202 IGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLIIG 242
           +GD+L+ V     +  +LE VTHE AVA LK+ ++ V L +G
Sbjct: 241 VGDRLLMV----NNYSLEEVTHEEAVAILKNTSEVVYLKVG 277
Score = 66.2 bits (160), Expect = 3e-09
Identities = 40/125 (32%), Positives = 64/125 (51%), Gaps = 11/125 (8%)
```



```
Query: 448 SPQPRQPGSRYASTNVLAAVPPGTPRAVSTEDITREPRTITIQKGPQGLGFNIVGGEDGQ 507
           SP   P    +T+ L +P     V+  +I E  IT+++G  GLGF+I GG D
Sbjct: 65  SPLKASPAPIIVNTDTLDTIP-----YVNGTEIEYEFEEITLERGNSGLGFSIAGGTDNP 119

Query: 508 ------GIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTL 561
                 GI+++ I+ GG A    L+  D +L VN V+++  +H +A +ALK +G + L
Sbjct: 120 HIGDDPGIFITKIIPGGAAAEDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARL 179

Query: 562 LAQYR 566
            + R
Sbjct: 180 YVRRR 184
Score = 65.5 bits (158), Expect = 5e-09
Identities = 38/81 (46%), Positives = 47/81 (57%), Gaps = 6/81 (7%)
```



```
Query: 487 ITIQKGPQGLGFNIVGGEDGQ------GIYVSFILAGGPADLGSELKRGDQLLSVNNVNL 540
           I + KGP+GLGF+I GG  Q      IYV+ I+ GG A    L+ GD+LL VNN +L
Sbjct: 194 IKLFKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIDGGAAQKDGRLQVGDRLLMVNNYSL 253

Query: 541 THATHEEAAQALKTSGGVVTL 561
               THEEA  LK +  VV L
Sbjct: 254 EEVTHEEAVAILKNTSEVVYL 274
Score = 50.8 bits (120), Expect = 1e-04
Identities = 33/87 (37%), Positives = 48/87 (54%), Gaps = 10/87 (11%)
```



```
Query: 154 EIDLVKGGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRAQVDGRLSIGDKLIAVRTNG 213
           ++ L KG  GLGF+I GG  +    GI+V+ +  GG A + G L  GD+++V NG
Sbjct: 421 KVVLHKGSTGLGFNIVGGEDGE------GIFVSFILAGGPADLSGELQRGDQILSV--NG 472

Query: 214 SEKNLENVTHELAVATLKSITDKVTLI 240
            +  L   +HE A A LK    VT+I
Sbjct: 473 ID--LRGASHEQAAAALKGAGQTVTII 497
Score = 41.2 bits (95), Expect = 0.10
Identities = 24/81 (29%), Positives = 36/81 (43%), Gaps = 6/81 (7%)
```



```
Query: 41  IQLERGNSGLGFSIAGGTDNPHIGTDTSIYITKLISGGAAAADGRLXXXXXXXXXXXXXXX 100
           + L +G++GLGF+I GG D       I+++ +++GG A   G L
Sbjct: 422 VVLHKGSTGLGFNIVGGEDG------EGIFVSFILAGGPADLSGELQRGDQILSVNGIDL 475

Query: 101 XXXPHASAVDALKKAGNVVKL 121
              H A  ALK AG  V +
Sbjct: 476 RGASHEQAAAALKGAGQTVTI 496
```

FIGURE 6D

CLUSTAL W (1.82) sequence alignment

```
Drosophila    ---------MTTRKKKRDGG----------------------------------------- 11
Human         MFFACYCALRTNVKKYRYQDEDAPHDHSLPRLTHEVRGPELVHVSEKNLSQIENVHGYVL 60
                       *. ** *   .

Drosophila    --------GSGGGFIKKVSSLFNLDSVNG-DDSWLYEDIQLERGNSGLGFSIAGGTDNPH 62
Human         QSHISPLKASPAPIIVNTDTLDTIPYVNGTEIEYEFEEITLERGNSGLGFSIAGGTDNPH 120
                       .* . :* :..:* .:   *** : .: :*:* ********************

Drosophila    IGTDTSIYITKLISGGAAAADGRLSINDIIVSVNDVSVVDVPHASAVDALKKAGNVVKLH 122
Human         IGDDPGIFITKIIPGGAAAEDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARLY 180
              ** *..*:***:*.***** **** :** *: **:*.* :*.*.:.**:***:**.:.:*:

Drosophila    VKRKRGTATTPAAGSAAGDARDSAASGPKVIEIDLVKGGKGLGFSIAGGIGNQHIPGDNG 182
Human         VRRRRPILET------------------VVEIKLFKGPKGLGFSIAGGVGNQHIPGDNS 221
              *.*:* *     *:**.*.** *********:*********.

Drosophila    IYVTKLTDGGRAQVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLIIG 242
Human         IYVTKIIDGGAAQKDGRLQVGDRLLMVNN----YSLEEVTHEEAVAILKNTSEVVYLKVG 277
              *****: *** ** ****.:**:*: *..    .**:**** *** **. :: * * :*

Drosophila    KTQHLTTSASGGGGGGLSSGQQLSQSQSQLATSQSQSQVHQQQHATPMVNSQSTGALNSM 302
Human         NPTTIYMTDPYGP-------PDITHS----------------YSPPMEN---------- 303
              :. : : . *        :::::*              ::.** *

Drosophila    GQTVVDSPSIPQAAAAVAAAANASASASVIASNNTISNTTVTTVTATATASNDSSKLPPS 362
Human         -------------------------HLLSGNN-------------GTLEYKTSLPPIS 323
                                       :::.**              .* . .:* * *

Drosophila    LGANSSISISNSNSNSNSNNINNINSINNNNSSSSSTTATVAAATPTAASAAAAAASSPP 422
Human         PGRYSPIPKHMLVDDDYTRPPEPVYSTVNKLCDKP--------ASPRHYSPVECDKSFLL 375
              * *.*.    .:. :.  : : * *: ....   *:*  *... *

Drosophila    ANSFYNNASMPALPVESNQTNNRSQSPQPRQPGSRYASTNVLAAVPPGTPRAVSTEDITR 482
Human         S-APYSHYHLGLLP-DSEMTSHSQHSTATRQP-------------SMTLQRAVSLE---G 417
              : : *.:  :  : **.:*: *.:  .:*. .***            **** *

Drosophila    EPRTITIQKGPQGLGFNIVGGEDGQGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTH 542
Human         EPRKVVLHKGSTGLGFNIVGGEDGEGIFVSFILAGGPADLSGELQRGDQILSVNGIDLRG 477
              ***.::.::**. ***********:**:************..**:****.****.::*

Drosophila    ATHEEAAQALKTSGGVVTLLAQYRPEEYNRFEARIQELKQQAALGAGGSGT-LLRTTQKR 601
Human         ASHEQAAAALKGAGQTVTIIAQYQPEDYARFEAKIHDLREQMMNHSMSSGSGSLRTNQKR 537
              *.**.** *** :* .**::***:**:* ****.*:.:*::*    : .**:  ***.***

Drosophila    SLYVRALFDYDPNRDDGLPSRGLPFKHGDILHVTNASDDEWWQARRVLGDNEDEQIGIVP 661
Human         SLYVRAMFDYDKSKDSGLPSQGLSFKYGDILHVINASDDEWWQARRVMLEGDSEEMGVIP 597
              ******:**** .:*.****:**.**:****** *************: :.:.*::*::*

Drosophila    SKRRWERKMRARDRSVKFQGHAAAANNNLDKQSTLDRKKKNFTFSRKFPFMKSRDEKNEDG 721
Human         SKRRVERKERARLKTVKFNAKPGVID--SKGSFNDKRKKSFIFSRKFPFYKNKEQSEQET 655
              **** *** *** ::***.:.... :  .* * *::**.* ******* *.:::.:::

Drosophila    SDQEPNGVVSSTSEIDINNVNNNQSNEPQPSEENVLSYEAVQRLSINYTRPVIILGPLKD 781
Human         SDPE----------------------RGQEDLILSYEPVTRQEINYTRPVIILGPMKD 691
              ** *                      : .*: :****.* .*.***********.**

Drosophila    RINDDLISEYPDKFGSCVPHTTRPKREYEVDGRDYHFVSSREQMERDIQNHLFIEAGQYN 841
Human         RINDDLISEFPDKFGSCVPHTTRPKRDYEVDGRDYHFVISREQMEKDIQEHKFIEAGQYN 751
              *********:*****************:***********:******:****:* ********

Drosophila    DNLYGTSVASVREVAEKGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRM 901
Human         DNLYGTSVQSVRFVAERGKHCILDVSGNAIKRLQVAQLYPIAIFIKPRSLESLMEMNKRL 811
              ******** *** ***:*********************:*:****:*::*:****.*:

Drosophila    TEEQAKKTYERAIKMEQEFGEYFTGVVQGDTIEEIYSKVKSMIWSQSGPTIWVPSKESL 960
Human         TEEQAKKTYDRAIKLEQEFGEYFTAIVQGDTLEDIYNQCKLVIEEQSGPFIWIPSKEKL 870
              *********:****:*********.:*****:*:**.: * :* .**** **:****.*
```

FIGURE 7

```
Hu-Dlg1   ---MPVRKQDTQRALHLLEEYRSKLSQTEDRQLRSSIERVINIFQSNLFQ-ALIDIQEFY 56
Hu-Dlg4   ---MSQRPRAPRSALWLLAPPLLRWAPP-----------LLTVLHSDLFQ-ALLDILDYY 45
Hu-Dlg2   ---MFFACYCALRTNVKKYRYQDEDAPHDHS--------LPRLTHEVRGP-ELVHVSEK- 47
Hu-Dlg3   MHKHQHCCKCPECYEVTRLAALRRLEPPGYG-----DWQVPDPYGPGGGNGASAGYGGYS 55
Dm-Dlg1   ---MTTRKK-------------------KRDGG--------------------- 11
Hu-Dlg5   --------------------------------------------------------


Hu-Dlg1   EVTLLDNPKCIDRSKPSEPIQPVNTWEISSLPSSTVTSETLPSSLSPSVEKYRYQDEDTP 116
Hu-Dlg4   EASLSES------------------------------------QKYRYQDEDTP 63
Hu-Dlg2   NLSQIEN------------------------------------VHGYVLQSHISP 66
Hu-Dlg3   SQTLPSQAG------------------------------------ATPTPRTKAKLIP 77
Dm-Dlg1   --------------------------------------------------------
Hu-Dlg5   --------------------------------------------------------


Hu-Dlg1   PQEHISPQITNEVIGPELVHVSEKNLSEIENVHGFVSHSHISPIKPTEAVLPSPPTVPVI 176
Hu-Dlg4   PLEHSP----------------------------------AHLPN------- 74
Hu-Dlg2   LK----------------------------------------------- 68
Hu-Dlg3   TGRDVG-------------------------------PVPLKPVPGK------ 93
Dm-Dlg1   --------------------------------------------------------
Hu-Dlg5   --------------------------------------------------------


Hu-Dlg1   PVLPVPAENTVILPTIPQANPPPVLVNTDSLETP---TYVNGTDADYEYEEITLERGNSG 233
Hu-Dlg4   ------------------QANSPPVIVNTDTLEAPGYELQVNGTEGEMEYEEITLERGNSG 117
Hu-Dlg2   ------------------ASPAPIIVNTDTLDTIP---YVNGTEIEYEFEEITLERGNSG 107
Hu-Dlg3   -----------STPKLNGSGPSWWPECTCTNRDWYEQVNGSDGMFKYEEIVLERGNSG 140
Dm-Dlg1   -----------------GSGGGFIKKVSSLFNLD---SVNGDD-SWLYEDIQLERGNSG 49
Hu-Dlg5   -------------------------------------MRATHGSNSLPSSARLGSSSN 21
                                          :... .      ..*.


Hu-Dlg1   LGFSIAGGTDNPHIGDDSSIFITKIITGGAAAQDGRLRVNDCILQVNEVDVRDVTHSKAV 293
Hu-Dlg4   LGFSIAGGTDNPHIGDDPSIFITKIIPGGAAAQDGRLRVNDSILFVNEVDVREVTHSAAV 177
Hu-Dlg2   LGFSIAGGTDNPHIGDDPGIFITKIIPGGAAAEDGRLRVNDCILRVNEVDVSEVSHSKAV 167
Hu-Dlg3   LGFSIAGGIDNPHVPDDPGIFITKIIPGGAAAMDGRLGVNDCVLRVNEVEVSEVVHSRAV 200
Dm-Dlg1   LGFSIAGGTDNPHIGTDTSIYITKLISGGAAAADGRLSINDIIVSVNDVSVVDVPHASAV 109
Hu-Dlg5   LQFKAER-IKIPSTPRYPRSVVGSER--GSVSHSECSTPPQSPLNIDTLSSCSQSQTSAS 78
          * *.      . *      . :.    *:.:  .    :  : ::  :.   ::  *


Hu-Dlg1   EALKEAGSIVRLYVKRRK------PVS-------------EKIMEIKLIKGPKGLGFSI 333
Hu-Dlg4   EALKEAGSIVRLYVMRRK------PPA-------------EKVMEIKLIKGPKGLGFSI 217
Hu-Dlg2   EALKEAGSIARLYVRRRR------PIL-------------ETVVEIKLFKGPKGLGFSI 207
Hu-Dlg3   EALKEAGPVVRLVVRRRQ------PPP-------------ETIMEVNLLKGPKGLGFSI 240
Dm-Dlg1   DALKKAGNVVKLHVKRKR-GTATTPAAGSAAGDARDSAASGPKVIEIDLVKGGKGLGFSI 168
Hu-Dlg5   TLPRIAVNPASLGERRKDR---PYV-------------EEPRHVKVQKGSEPLGISI 119
          : *   . *   *:             .:.:  **  :  **:**


Hu-Dlg1   AGGVGNQHIPGDNSIYVTKIIEGGAAHKDGKLQIGDKLLAVNN----VCLEEVTHEEAVT 389
Hu-Dlg4   AGGVGNQHIPGDNSIYVTKIIEGGAAHKDGRLQIGDKILAVNS----VGLEDVMHEDAVA 273
Hu-Dlg2   AGGVGNQHIPGDNSIYVTKIIDGGAAQKDGRLQVGDRLLMVNN----YSLEEVTHEEAVA 263
Hu-Dlg3   AGGIGNQHIPGDNSIYITKIIEGGAAQKDGRLQIGDRLLAVNN----TNLQDVRHEEAVA 296
Dm-Dlg1   AGGIGNQHIPGDNGIYVTKLTDGGRAQVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVA 228
Hu-Dlg5   VSGE-------KGGIYVSKVTVGSIAHQAG-LEYGDQLLEFNG----INLRSATEQQARL 167
          ..*       ...**::*:  *. *:  * *. **::: ..    *... .: *


Hu-Dlg1   ALKNTSDFVYLKVAKPTSMYMNDGYA---------------------------- 415
Hu-Dlg4   ALKNTYDVVYLKVAKPSNAYLSDSYA---------------------------- 299
Hu-Dlg2   ILKNTSEVVYLKVGNPTTIYMTDPYG---------------------------- 289
Hu-Dlg3   SLKNTSDMVYLKVAKPGSLHLNDMYA---------------------------- 322
Dm-Dlg1   TLKSITDKVTLIIGKTQHLTTSASGGGGGGGLSSGQQLSQSQSQLATSQSQSQVHQQQHAT 288
Hu-Dlg5   IIGQQCDTITILAQYNPHVHQLSSHS---------------------------- 193
          : .  : : :      .


Hu-Dlg1   --------------------------------------------------------
Hu-Dlg4   --------------------------------------------------------
Hu-Dlg2   ---------------------------------------------------------
Hu-Dlg3   --------------------------------------------------------
Dm-Dlg1   PMVNSQSTGALNSMGQTVVDSPSIPQAAAAVAAAANASASASVIASNNTISNTTVTTVTA 348
```

```
Hu-Dlg5       --------------------------------------------------------------

Hu-Dlg1       -----------PP--------DITNSSSQPVDNHVS-------PSSFLG----------- 438
Hu-Dlg4       -----------PP--------DITTSYSQHLDNEIS-------HSSYLGTD-------YP 326
Hu-Dlg2       -----------PP--------DITHSYSPPMENHLL-------SGNNGTLE-------YK 316
Hu-Dlg3       -----------PP--------DYASTFTALADNHIS-------HNSSLGYLGAVESKVSY 356
Dm-Dlg1       TATASNDSSKLPPSLGANSSISISNSNSNSNNINNNINSINNNNSSSSSTTATVAAATP 408
Hu-Dlg5       --------------------RSSSHLDPAGTHSTLQ-----GSGTTTPEHPSVIDPLM 226
                                  :   :          ..                ..

Hu-Dlg1       --QTPASPARYSPVSKAVLGDDEITR---------------------------------- 462
Hu-Dlg4       TAMTPTSPRRYSPVAKDLLGEEDIPR---------------------------------- 352
Hu-Dlg2       TSLPPISPGRYSPIPKHMLVDDDYTRPPEPVYSTVNKLCDKPASPRHYSPVECDKSFLLS 376
Hu-Dlg3       PAPPQVPPTRYSPIPRHMLAEEDFTR---------------------------------- 382
Dm-Dlg1       TAASAAAAAASSPPANSFYNNASMPALPVESNQTNNRSQSPQPRQPGSRYASTN------ 462
Hu-Dlg5       EQDEGPSTPPAKQSSSRIAGDANKKT----------:----------------------- 252
                         ..    .   .   :  .

Hu-Dlg1       ------------------------------------------EPRKVVLHRGSTGLGFNIV 481
Hu-Dlg4       ------------------------------------------EPRRIVIHRGSTGLGFNIV 371
Hu-Dlg2       APYSHYHLGLLPDSEMTSHSQHSTATRQPSMTLQRAVSLEGEPRKVVLHKGSTGLGFNIV 436
Hu-Dlg3       ------------------------------------------EPRKIILHKGSTGLGFNIV 401
Dm-Dlg1       ----------------------VLAAVPPGTPRAVSTEDITREPRTITIQKGPQGLGFNIV 501
Hu-Dlg5       ------------------------------------------LEPRVVFIKKSQLELGVHLC 272
                                                        *** : :::. **.::

Hu-Dlg1       GGEDGEGIFISFILAGGPADLSGELRKGDRIISVNSVDLRAASHEQAAAALKNAGQAVTI 541
Hu-Dlg4       GGEDGEGIFISFILAGGPADLSGELRKGDQILSVNGVDLRNASHEQAAIALKNAGQTVTI 431
Hu-Dlg2       GGEDGEGIFVSFILAGGPADLSGELQRGDQILSVNGIDLRGASHEQAAAALKGAGQTVTI 496
Hu-Dlg3       GGEDGEGIFVSFILAGGPADLSGELRRGDRILSVNGVNLRNATHEQAAAALKRAGQSVTI 461
Dm-Dlg1       GGEDGQGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTL 561
Hu-Dlg5       GG-NLHGVFVAEVEDDSPAKGPDGLVPGDLILEYGSLDVRNKTVEEVYVEMLKPRDGVRL 331
              ** : .*::::: :   ..**.  .  *  **  ::.  ..::   : *:.   :  .  * :

Hu-Dlg1       VAQYRPEEYSRFEAKIHDLREQMMNSSISSGSGSLRTSQKRSLYVRALFDYDKTKDSGLP 601
Hu-Dlg4       IAQYKPEEYSRFEAKIHDLREQLMNSSLGSGTASLRSNPKRGFYIRALFDYDKTKDCGFL 491
Hu-Dlg2       IAQYQPEDYARFEAKIHDLREQMMNHSMSSGSGSLRTNQKRSLYVRAMFDYDKSKDSGLP 556
Hu-Dlg3       VAQYRPEEYSRFESKIHDLREQMMNSSMSSGSGSLRTSEKRSLYVRALFDYDRTRDSCLP 521
Dm-Dlg1       LAQYRPEEYNRFEARIQELKQQAALGAGGSGT-LLRTTQKRSLYVRALFDYDPNRDDGLP 620
Hu-Dlg5       KVQYRPEEFTKAKG---------------------LPGDSFYIRALYDR-----LADV 363
              .**:**:: : :.                       .:*:**::*

Hu-Dlg1       SQGLNFKFGDILHVINASDD---EWWQARQVTPDGESDEVGVIPSKRRVEKKERARLKTV 658
Hu-Dlg4       SQALSFRFGDVLHVIDASDE---EWWQARRVHSDSETDDIGFIPSKRRVERREWSRLKAK 548
Hu-Dlg2       SQGLSFKYGDILHVINASDD---EWWQARRVMLEGDSEEMGVIPSKRRVERKERARLKTV 613
Hu-Dlg3       SQGLSFSYGDILHVINASDD---EWWQARLVTPHGESEQIGVIPSKKRVEKKERARLKTV 578
Dm-Dlg1       SRGLPFKHGDILHVTNASDD---EWWQARRVLGDNEDEQIGIVPSKRRWERKMRARDRSV 677
Hu-Dlg5       EQELSFKKDDILYVDDTLPQGTFGSWMAWQLDENAQKIQRGQIPSKYVMDQEFSRRLSMS 423
              .: * *  .*:*:* :: :      * *  :  . : : * :***  ::.   *

Hu-Dlg1       KFNSKT-----RDKGQSFNDKRKKNLFSRKFPFYKNKDQSEQETSDADQH---------- 703
Hu-Dlg4       DWG--------------------------------------------------------- 551
Hu-Dlg2       KFNAKPGVI--DSKGSFNDKRKKSFIFSRKFPFYKNKEQSEQE---------------- 654
Hu-Dlg3       KFHARTGMI--ESNRDFPGLSDDYY---------------------------------- 601
Dm-Dlg1       KFQGHAAANNNLDKQSTLDRKKKNFTFSRKFPFMKSRDEKNEDGSDQEPNGVVSSTSEID 737
Hu-Dlg5       EVKDDNSATKTLSAAAARRSFFRRKHKHKRSGSKDGKDLLALDAFS-------------- 468
                .

Hu-Dlg1       VTSNASDSESSYRGQEEYVLSYEPVNQQEVNYTRPVIILGPMKDRINDDLISEFPDKFGS 763
Hu-Dlg4       -------SSSGSQGREDSVLSYETVTQMEVHYARPIIILGPTKDRANDDLLSEFPDKFGS 604
Hu-Dlg2       -------TSDPERGQEDLILSYEPVTRQEINYTRPVIILGPMKDRINDDLISEFPDKFGS 707
Hu-Dlg3       -------GAKNLKGQEDAILSYEPVTRQEIHYARPVIILGPMKDRVNDDLISEFPHKFGS 654
Dm-Dlg1       INNVNNNQSNEPQPSEENVLSYEAVQRLSINYTRPVIILGPLKDRINDDLISEYPDKFGS 797
Hu-Dlg5       -------SDSIPLFEDSVSLAYQRVQKVDCTALRPVLILGPLLDVVKEMLVNEAPGKFCR 521
                      .   :.  *:*:  * : .   **:*:**** *  :: *:.* * **

Hu-Dlg1       CVPHTTRPKRDYEVDGRDYHFVTSREQMEKDIQEHKFIEAGQYNNHLYGTSVQSVREVAG 823
Hu-Dlg4       CVPHTTRPKREYEIDGRDYHFVSSREKMEKDIQAHKFIEAGQYNSHLYGTSVQSVREVAE 664
Hu-Dlg2       CVPHTTRPKRDYEVDGRDYHFVISREQMEKDIQEHKFIEAGQYNDNLYGTSVQSVRFVAE 767
Hu-Dlg3       CVPHTTRPRRDNEVDGQDYHFVVSREQMEKDIQDNKFIEAGQFNDNLYGTSIQSVRAVAE 714
Dm-Dlg1       CVPHTTRPKREYEVDGRDYHFVSSREQMERDIQNHLFIEAGQYNDNLYGTSVASVREVAE 857
Hu-Dlg5       CPLEVMK---------------ASQQAIERGVKDCLFVDYKRRSGHFDVTTVASIXEITE 566
```

```
                 *  .. :              *:: :*:.::  *::  : ..::  *:: *:  ::
Hu-Dlg1   KGKHCILDVSGNAIKRLQIAQLYPISIFIKPKSMENIMEMNK------RLTEEQARKTFE 877
Hu-Dlg4   QGKHCILDVSANAVRRLQAAHLHPIAIFIRPRSLENVLEINK------RITEEQARKAFD 718
Hu-Dlg2   RGKHCILDVSGNAIKRLQVAQLYPIAIFIKPRSLESLMEMNK------RLTEEQAKKTYD 821
Hu-Dlg3   RGKHCILDVSGNAIKRLQQAQLYPIAIFIKPKSIEALMEMNR------RQTYEQANKIYD 768
Dm-Dlg1   KGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNR------RMTEEQAKKTYE 911
Hu-Dlg5   KNRHCLLDIAPHAIERLHHMHIYPIVIFIHYKSAKHIKEQRDPIYLRDKVTQRHSKEQFE 626
          :.:**:**::  :*:.**:  :::*: :**: :* . : * .        : *  .:.: ::


Hu-Dlg1   RAMKLEQEFTEHFTAIVQGDTLEDIYNQVKQIIEEQSGSYIWVPAKEKL 926
Hu-Dlg4   RATKLEQEFTECFSAIVEGDSFEEIYHKVKRVIEDLSGPYIWVPARERL 767
Hu-Dlg2   RAIKLEQEFGEYFTAIVQGDTLEDIYNQCKLVIEEQSGPFIWIPSKEKL 870
Hu-Dlg3   KAMKLEQEFGEYFTAIVQGDSLEEIYNKIKQIIEDQSGHYIWVPSPEKL 817
Dm-Dlg1   RAIKMEQEFGEYFTGVVQGDTIEEIYSKVKSMIWSQSGPTIWVPSKESL 960
Hu-Dlg5   AAQKLEQEYSRYFTGVIQGGALSSICTQILAMVNQEQNKVLWIPACPL- 674
           *  *:***: . *:.:::*.::..*  :   ::  . ..  :*:*:
```
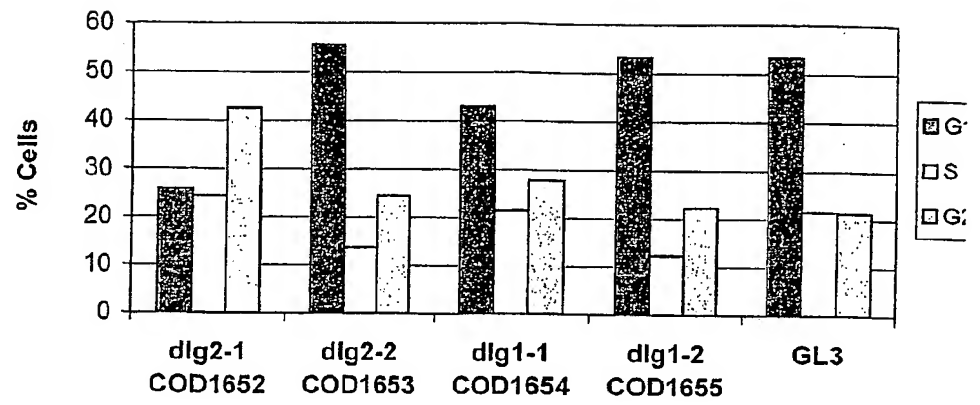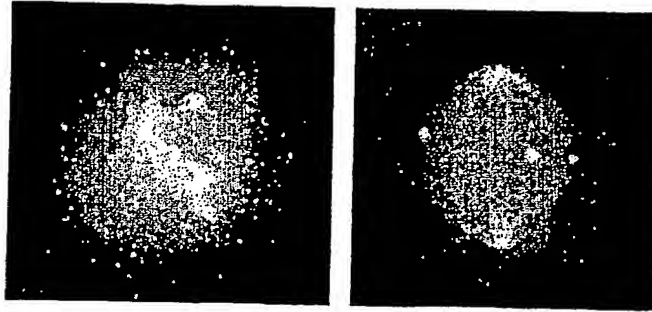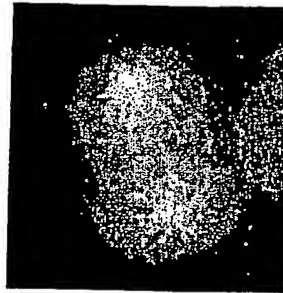
FIGURE 8

FIGURE 9

A

B

FIGURE 10

A

B